

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 2, 2002, 01:32:29 ; Search time 170.806 Seconds
(without alignments)
822.965 Million cell updates/sec

Title: US-09-856-979-7
Perfect score: 365
Sequence: 1 tcagccagaccaatgggggc.....tccatcaagccgtcgcatg 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues 683086
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Published_Applications_NA.*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	365	100.0	5349	10	US-09-970-921-7	Sequence 7, Appli
2	365	100.0	6539	9	US-09-509-945-5	Sequence 5, Appli
3	365	100.0	6548	9	US-09-509-945-4	Sequence 4, Appli
4	35	9.6	1241	12	US-10-044-090-274	Sequence 274, App
5	31.6	8.7	918	10	US-09-815-242-9784	Sequence 9784, Ap
6	31.2	8.5	385	10	US-09-783-590-6496	Sequence 6496, Ap
7	31	8.5	587	10	US-09-878-574-4548	Sequence 4548, Ap
8	30.6	8.4	300	10	US-09-294-093B-3715	Sequence 3715, Ap
9	30.6	8.4	436	10	US-09-728-445-698	Sequence 698, App
10	30.6	8.4	1623	9	US-09-712-363-23	Sequence 23, Appl
11	30.6	8.4	2073	9	US-10-068-059-9	Sequence 9, Appli
12	30.6	8.4	2130	9	US-10-068-059-7	Sequence 7, Appli
13	30.6	8.4	2175	9	US-10-068-059-11	Sequence 11, Appl
14	30.6	8.4	2241	9	US-10-068-059-5	Sequence 5, Appli
15	30.4	8.3	3466	10	US-09-938-405-1	Sequence 1, Appli
16	30.2	8.3	264	10	US-09-923-876-4605	Sequence 4605, Ap
17	30.2	8.3	155074	9	US-10-026-188-6	Sequence 6, Appli
18	30	8.2	4450	10	US-09-764-887-497	Sequence 497, App
19	30	8.2	4454	10	US-09-764-887-496	Sequence 496, App

c	20	30	8.2	80959	9	US-09-858-546-3	Sequence 3, Appli
	21	29.8	8.2	1436	10	US-09-788-345-11	Sequence 11, Appl
	22	29.8	8.2	10144	10	US-09-880-107-2168	Sequence 2168, Ap
	23	29.6	8.1	363	10	US-09-878-574-1890	Sequence 1890, Ap
	24	29.6	8.1	170834	10	US-09-835-232-7	Sequence 7, Appli
c	25	29.4	8.1	1203	9	US-09-945-182-29	Sequence 29, Appl
	26	29.4	8.1	41907	10	US-09-967-013-5	Sequence 5, Appli
c	27	29.2	8.0	165	10	US-09-878-574-14392	Sequence 14392, A
c	28	29.2	8.0	3715	10	US-09-880-107-2300	Sequence 2300, Ap
	29	29	7.9	1505	12	US-10-006-867-127	Sequence 127, App
	30	29	7.9	1505	12	US-10-052-586-377	Sequence 377, App
	31	29	7.9	1909	10	US-09-796-089-2	Sequence 2, Appli
	32	29	7.9	8911	10	US-09-764-853-895	Sequence 895, App
c	33	28.8	7.9	453	10	US-09-783-590-5627	Sequence 5627, Ap
c	34	28.6	7.8	446	10	US-09-864-761-20699	Sequence 20699, A
	35	28.6	7.8	855	10	US-09-764-853-104	Sequence 104, App
c	36	28.6	7.8	1061	9	US-09-990-415A-3	Sequence 3, Appli
c	37	28.6	7.8	1147	10	US-09-756-186-5	Sequence 5, Appli
c	38	28.6	7.8	1232	9	US-09-990-415A-1	Sequence 1, Appli
	39	28.6	7.8	1471	10	US-09-764-869-455	Sequence 455, App
	40	28.6	7.8	1635	10	US-09-864-761-20241	Sequence 20241, A
	41	28.6	7.8	1973	10	US-09-864-761-3471	Sequence 3471, Ap
	42	28.4	7.8	314	10	US-09-864-761-32286	Sequence 32286, A
	43	28.4	7.8	469	10	US-09-864-761-15780	Sequence 15780, A
c	44	28.4	7.8	2326	9	US-09-945-901-41	Sequence 41, Appl
c	45	28.4	7.8	2326	9	US-10-007-747-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-970-921-7
; Sequence 7, Application US/09970921
; Patent No. US20020133845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "T-DNA of pTTS243"
; NAME/KEY: misc_feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: label = RB, "T-DNA right border"
; NAME/KEY: misc_feature
; LOCATION: Complement((98)..(331))
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc_feature
; LOCATION: Complement((332)..(883))
; OTHER INFORMATION: label = bar, "region coding for phosphinthrincin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc_feature
; LOCATION: Complement((884)..(2258))
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; NAME/KEY: misc_feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc_feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"
; NAME/KEY: misc_feature

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; LOCATION: (4246)..(4577)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
; NAME/KEY: misc_feature
; LOCATION: Complement((5325)..(5349))
; OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7

Query Match      100.0%; Score 365; DB 10; Length 5349;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
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Db 3608 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 3667

QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3668 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 3727

QY 121 ATGGACGGGACAACTTCTTTTCAACCGTCTACTGCTACATCCTGTAGACGGTGGACGG 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3728 ATGGACGGGACAACTTCTTTTCAACCGTCTACTGCTACATCCTGTAGACGGTGGACGG 3787

QY 181 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGCACCGTTCGACCG 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3788 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGCACCGTTCGACCG 3847

QY 241 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGCGCTACAAAAGCCACACGCGCAG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3848 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGCGCTACAAAAGCCACACGCGCAG 3907

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3908 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 3967

QY 361 CGATG 365
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Db 3968 CGATG 3972

RESULT 2
US-09-509-945-5/c
; Sequence 5, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 6539
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pTS431
US-09-509-945-5

Query Match      100.0%; Score 365; DB 9; Length 6539;
Best Local Similarity 100.0%; Pred. No. 8e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
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Db 2977 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 2918

QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2917 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 2858
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QY 121 ATGACGGGACAAACACTTCTTTCAACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGG 180
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Db 2857 ATGACGGGACAAACACTTCTTTCAACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGG 2798

QY 181 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGGCAGCGTTCGACCG 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2797 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGGCAGCGTTCGACCG 2738

QY 241 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2737 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2678

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
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Db 2677 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2618

QY 361 CGATG 365
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Db 2617 CGATG 2613

RESULT 3
US-09-509-945-4/c
; Sequence 4, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID G
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pTS172
US-09-509-945-4

Query Match      100.0%; Score 365; DB 9; Length 6548;
Best Local Similarity 100.0%; Pred. No. 8e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
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Db 2986 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 2927

QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 120
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Db 2926 TCCTACACTCAACCTAACTGTTGAACGGTCTGTTCTGGCCACGGTGAGAAATGCACCTA 2867

QY 121 ATGACGGGACAAACACTTCTTTCAACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGG 180
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Db 2866 ATGACGGGACAAACACTTCTTTCAACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGG 2807

QY 181 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGGCAGCGTTCGACCG 240
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Db 2806 TGAGGTGCTTTCGCCATGACCGTCCTTGGTGTGCAGTCACTTGGCAGCGTTCGACCG 2747

QY 241 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2746 TGACTCACTGCGCACATTTGCCCGCGCGTCCGGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2687

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2686 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2627

QY 361 CGATG 365
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RESULT 10
US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match      8.4%; Score 30.6; DB 9; Length 1623;
Best Local Similarity 58.1%; Pred. No. 1.1;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCCCTAC 282
Db 1313 TTGGCGCGGTGCGCTCGTCCCTTCGAGCTTCGAGCTTCAGCTCGTCCAGGGTCGGGGCGCGCTTGC 1254

QY 283 AAAAGCCACACACGCGCGCGCGCCACGATAACC 315
Db 1253 AACAGCGTCACACCCCCACCGCGGACGATGCC 1221

RESULT 11
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 1623;
Best Local Similarity 58.1%; Pred. No. 1.1;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCCCTAC 282
Db 1313 TTGGCGCGGTGCGCTCGTCCCTTCGAGCTTCGAGCTTCAGCTCGTCCAGGGTCGGGGCGCGCTTGC 1254

QY 283 AAAAGCCACACACGCGCGCGCGCCACGATAACC 315
Db 1253 AACAGCGTCACACCCCCACCGCGGACGATGCC 1221

RESULT 12
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 2130;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCCCTAC 282
Db 1820 TTGGCGCGGTGCGCTCGTCCCTTCGAGCTTCAGCTCGTCCAGGGTCGGGGCGCGCTTGC 1761

QY 283 AAAAGCCACACACGCGCGCGCGCCACGATAACC 315
Db 1760 AACAGCGTCACACCCCCACCGCGGACGATGCC 1728

RESULT 13
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      8.4%; Score 30.6; DB 9; Length 2073;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCCCTAC 282
Db 1763 TTGGCGCGGTGCGCTCGTCCCTTCGAGCTTCAGCTCGTCCAGGGTCGGGGCGCGCTTGC 1704

QY 283 AAAAGCCACACACGCGCGCGCGCCACGATAACC 315
Db 1703 AACAGCGTCACACCCCCACCGCGGACGATGCC 1671

RESULT 12
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 2130;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCCCTAC 282
Db 1820 TTGGCGCGGTGCGCTCGTCCCTTCGAGCTTCAGCTCGTCCAGGGTCGGGGCGCGCTTGC 1761

QY 283 AAAAGCCACACACGCGCGCGCGCCACGATAACC 315
Db 1760 AACAGCGTCACACCCCCACCGCGGACGATGCC 1728

RESULT 13
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match      8.4%; Score 30.6; DB 9; Length 2175;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGCAGCTTGACCGTGACTGACTGACCTGCCACATTGCCCGCGCGTCCGCGGCGCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1865 TTGGCGCGGTGCGCTCGTGGCTTCGAGCTTCAGCTCGTCCAGGGTGGGGCGCGCTTGC 1806

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1805 AACAGCGTCACACCCCCACCGCGGACGATGCC 1773

RESULT 14
US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match      8.4%; Score 30.6; DB 9; Length 2241;
Best Local Similarity 58.1%; Pred. No. 1.4;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGCAGCTTGACCGTGACTGACTGACCTGCCACATTGCCCGCGCGTCCGCGGCGCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1931 TTGGCGCGGTGCGCTCGTGGCTTCGAGCTTCAGCTCGTCCAGGGTGGGGCGCGCTTGC 1872

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1871 AACAGCGTCACACCCCCACCGCGGACGATGCC 1839

RESULT 15
US-09-938-405-1
; Sequence 1, Application US/09938405
; Patent No. US20020111296A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/09/938,405
; CURRENT FILING DATE: 2001-08-23
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; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(1875)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (205)...()
; OTHER INFORMATION:
US-09-938-405-1

Query Match      8.3%; Score 30.4; DB 10; Length 3466;
Best Local Similarity 63.9%; Pred. No. 2;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 222 CTTGGGCACGCTTGACCGTGACTGACTGACCTGCCACATTGCCCGCGCGTCCGCGGCGCTA 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 CCTGTGCCCCCTCTGCTCCGGCACGGCCCTGTGCGCAGTGCCCGCGGCTTCCCCCGGCGCTG 129

QY 282 CAAAAGCCACAC 293
    || | | | |
Db 130 CACGCGGCGCGC 141

Search completed: December 2, 2002, 04:18:35
Job time : 179.806 secs
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